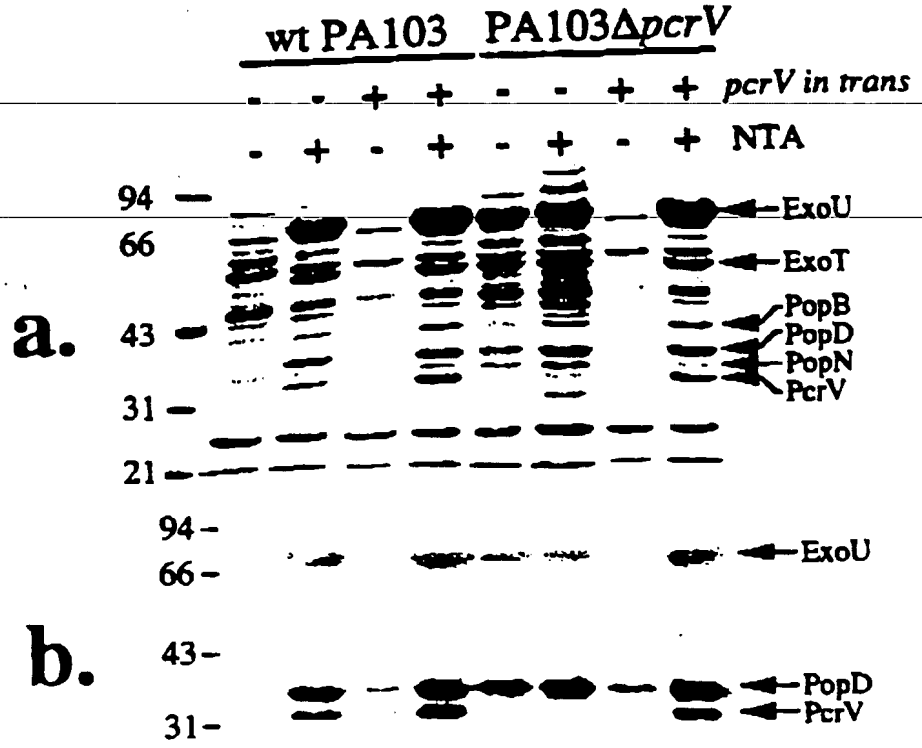
wt PA103
PA103ΔpcrV
- - + + - - + + pcrV in trans
- + - + - + - + NTA
94
66
43
31
21
ExoU
ExoT
PopB
PopD
PopN
PcrV
a.
94
66
ExoU
43
31
PopD
PcrV
b.

FIG. 1

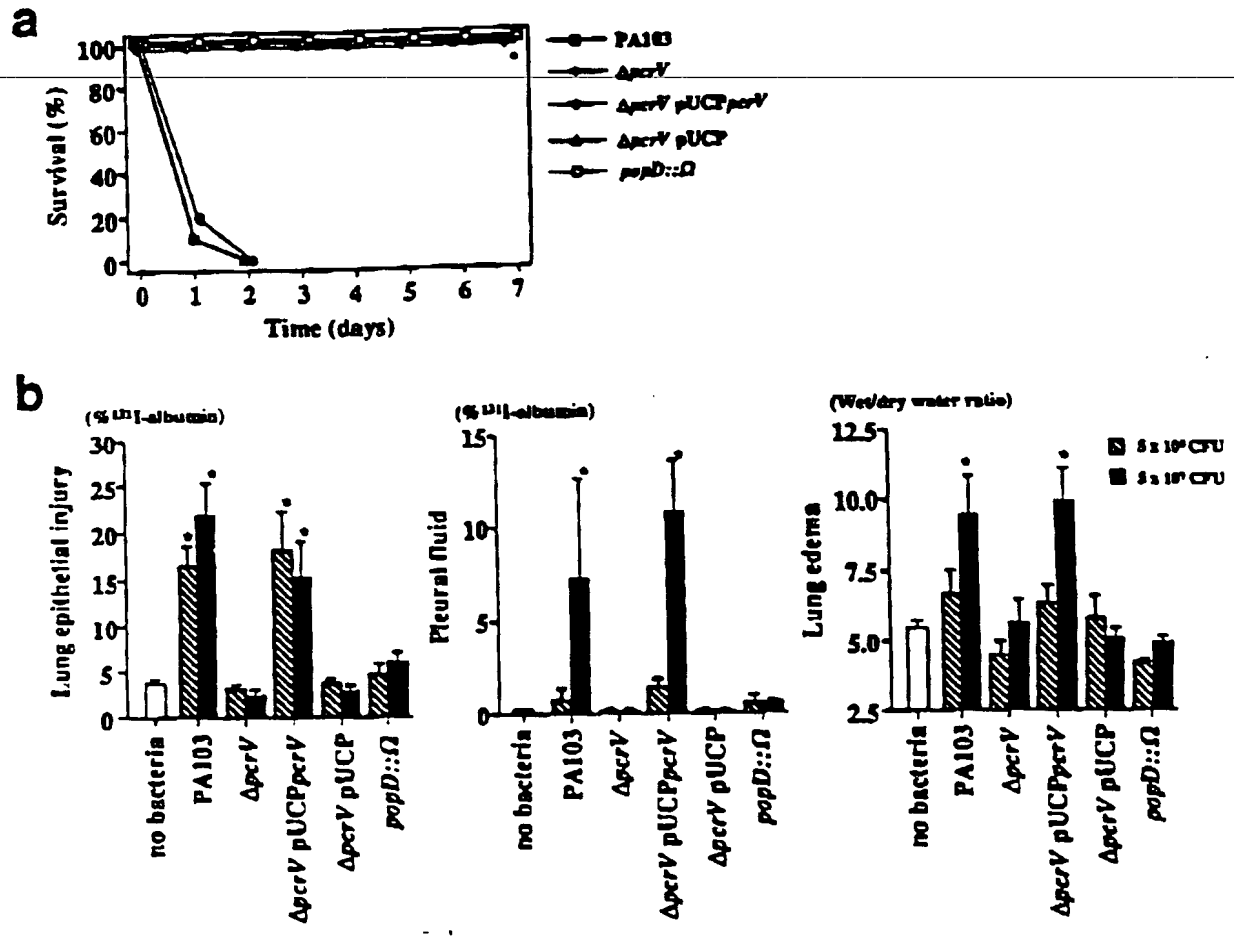
a
Survival (%)
Time (days)
PA103
ΔpcrV
ΔpcrV pUCPpcrV
ΔpcrV pUCP
popD::Ω
b
Lung epithelial injury
Pleural fluid
Lung edema
no bacteria
PA103
ΔpcrV
ΔpcrV pUCPpcrV
ΔpcrV pUCP
popD::Ω

FIG. 2

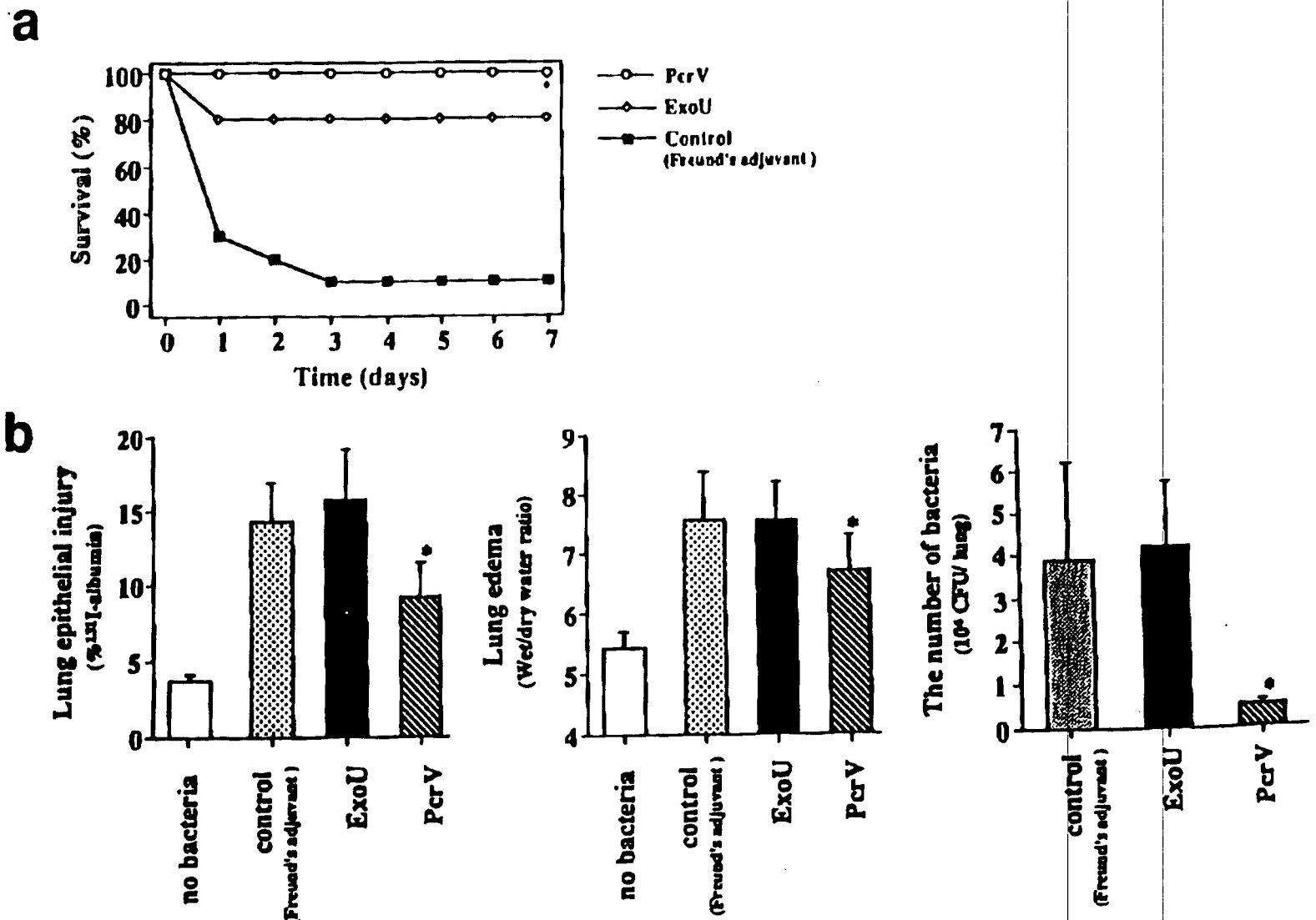

FIG. 3

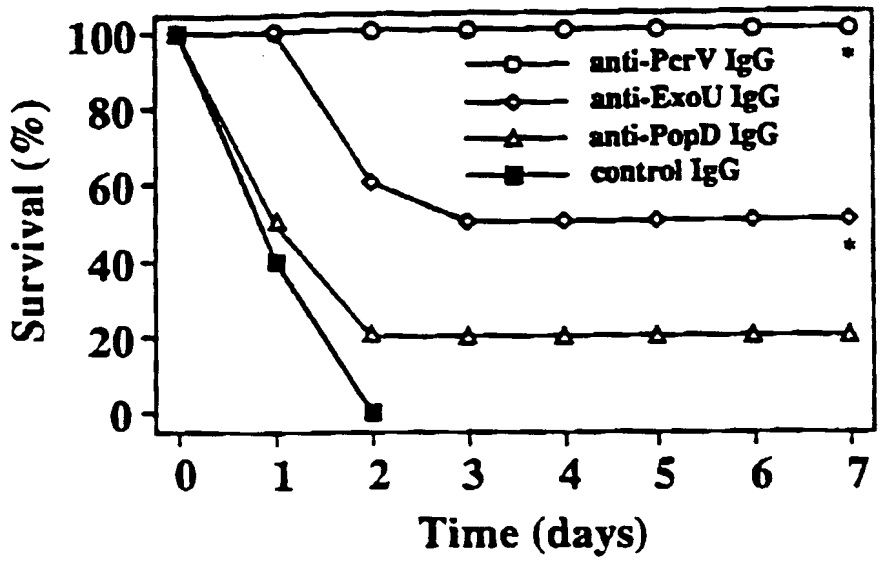
100
80
60
40
20
0
Survival (%)
0
1
2
3
4
5
6
7
Time (days)
anti-PcrV IgG
anti-ExoU IgG
anti-PopD IgG
control IgG
*
*

FIG. 4

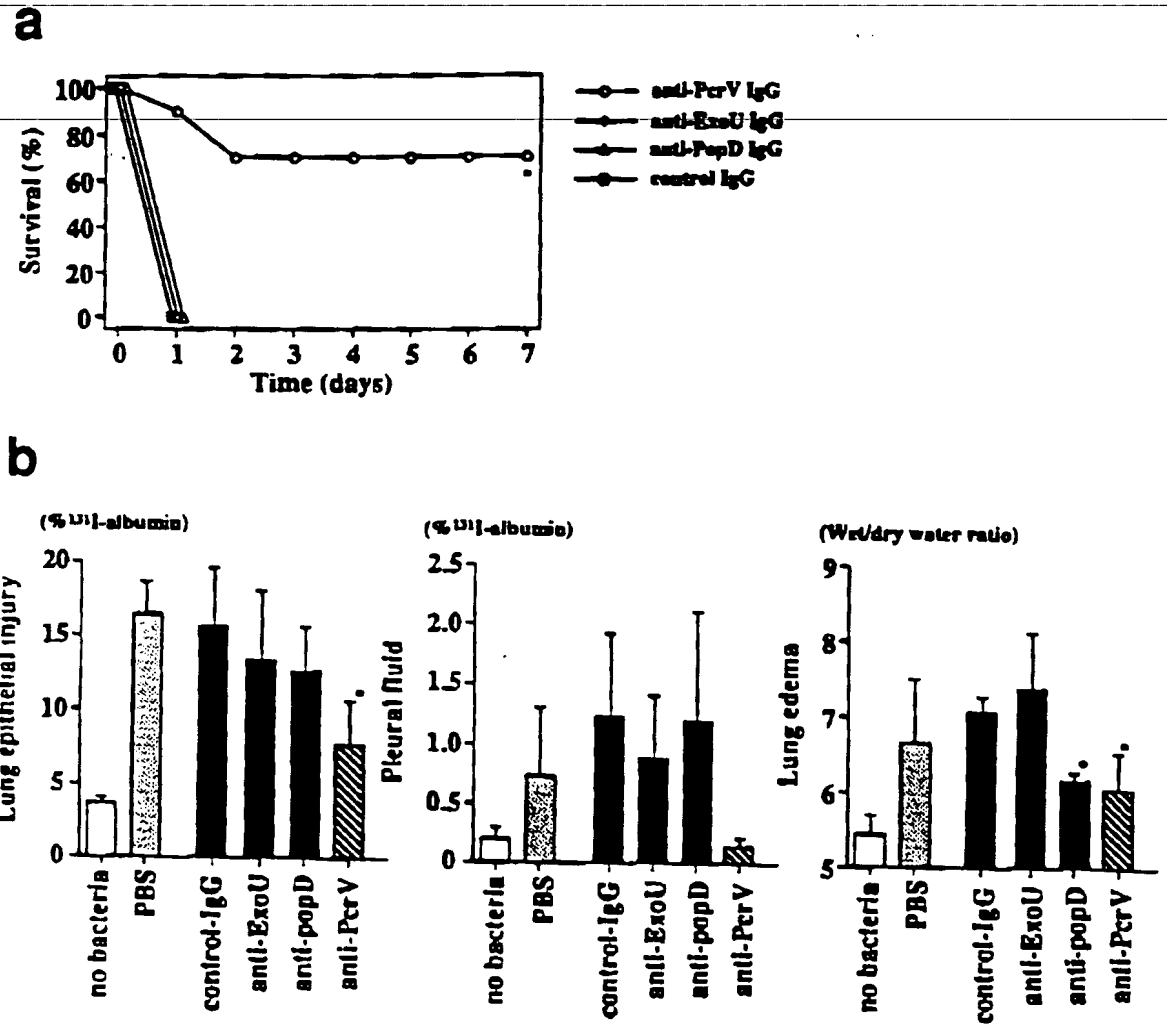
a
100
80
60
40
20
0
Survival (%)
0 1 2 3 4 5 6 7
Time (days)
anti-PcrV IgG
anti-ExoU IgG
anti-PopD IgG
control IgG
b
(%[131]-albumin)
Lung epithelial injury
20
15
10
5
0
no bacteria
PBS
control-IgG
anti-ExoU
anti-popD
anti-PcrV
(%[131]-albumin)
Pleural fluid
2.5
2.0
1.5
1.0
0.5
0
(Wet/dry water ratio)
Lung edema
9
8
7
6
5

FIG. 5

m166 heavy chain

1. m166 heavy chain (IgG2b) complete mRNA sequence:

(From the transcriptional start point to the polyA-tail)

```
CCATCCTCTT CTCATAGAGC CTCCATCAGA GCATGGCTGT CTTGGGGCTG
CTCTTCTGCC TGGTGACATT CCCAAGCTGT GTCCTATCCC AGGTGCAGCT
GAAGCAGTCA GGACCTGGCC TAGTGCAGCC CTCACAGAGC CTGTCCATCA
CCTGCACAGT CTCTGGTTTC TCATTAACTA GCTATGGTGT ACACTGGGTT
CGTCAGTCTC CAGGAAAGGG TCTGGAGTGG CTGGGAGTGA TATGGAGTGG
TGGAGACACA GACTATAATG CAGCTTTCAT ATCCAGACTG AGCATCAGCA
AGGACAATTC CAAGAGCCAA CTCTTCTTTA AAATGAACAG TCTGCGAGCT
ACTGACACAG CCATATATTA CTGTGCCAGA AATAGAGGGG ATATTTACTA
TGATTTCACT TATGCCATGG ACTACTGGGG TCAAGGAACC TCAGTCACCG
TCTCCTCAGC CAAAACAACA CCCCCATCAG TCTATCCACT GGCCCCTGGG
TGTGGAGATA CAACTGGTTC CTCCGTGACT CTGGGATGCC TGGTCAAGGG
CTACTTCCCT GAGTCAGTGA CTGTGACTTG GAACTCTGGA TCCCTGTCCA
GCAGTGTGCA CACCTTCCCA GCTCTCCTGC AGTCTGGACT CTACACTATG
AGCAGCTCAG TGACTGTCCC CTCCAGCACC TGGCCAAGTC AGACCGTCAC
CTGCAGCGTT GCTCACCCAG CCAGCAGCAC CACGGTGGAC AAAAAACTTG
AGCCCAGCGG GCCCATTTCA ACAATCAACC CCTGTCCTCC ATGCAAGGAG
TGTCACAAAT GCCCAGCTCC TAACCTCGAG GGTGGACCAT CCGTCTTCAT
CTTCCCTCCA AATATCAAGG ATGTACTCAT GATCTCCCTG ACACCCAAGG
TCACGTGTGT GGTGGTGGAT GTGAGCGAGG ATGACCCAGA CGTCCAGATC
AGCTGGTTTG TGAACAACGT GGAAGTACAC ACAGCTCAGA CACAAACCCA
TAGAGAGGAT TACAACAGTA CTATCCGGGT GGTCAGCACC CTCCCCATCC
AGCACCAGGA CTGGATGAGT GGCAAGGAGT TCAAATGCAA GGTCAACAAC
AAAGACCTCC CATCACCCAT CGAGAGAACC ATCTCAAAAA TTAAAGGGCT
AGTCAGAGCT CCACAAGTAT ACATCTTGCC GCCACCAGCA GAGCAGTTGT
CCAGGAAAGA TGTCAGTCTC ACTTGCCTGG TCGTGGGCTT CAACCCTGGA
GACATCAGTG TGGAGTGGAC CAGCAATGGG CATACAGAGG AGAACTACAA
GGACACCGCA CCAGTCCTGG ACTCTGACGG TTCTTACTTC ATATATAGCA
AGCTCAATAT GAAAACAAGC AAGTGGGAGA AAACAGATTC CTTCTCATGC
AACGTGAGAC ACGAGGGTCT GAAAAATTAC TACCTGAAGA AGACCATCTC
CCGGTCTCCG GGTAAATGAG CTCAGCACCC ACAAAGCTCT CAGGTCCTAA
GAGACACTGG CACCCATATC CATGCATCCC TTGTATAAAT AAAGCATCCA
GCAAAGCCTG GTACCATGTA AAAAAAAAAA AAAAAAAA
```

FIG. 6A

2. m166 heavy chain (IgG2b) complete amino acid sequence:

(From the start coden to the stop codon)

```
**********************************************************************
MAVLGLLFCL VTFPSCVLSQ VQLKQSGPGL VQPSQSLSIT CTVSGFSLTS
YGVHWVRQSP GKGLEWLGVI WSGGDTDYNA AFISRLSISK DNSKSQLFFK
MNSLRATDTA IYYCARNRGD IYYDFTYAMD YWGQGTSVTV SSAKTTPPSV
YPLAPGCGDT TGSSVTLGCL VKGYFPESVT VTWNSGSLSS SVHTFPALLQ
SGLYTMSSSV TVPSSTWPSQ TVTCSVAHPA SSTTVDKKLE PSGPISTINP
CPPCKECHKC PAPNLEGGPS VFIFPPNIKD VLMISLTPKV TCVVVDVSED
DPDVQISWFV NNVEVHTAQT QTHREDYNST IRVVSTLPIQ HQDWMSGKEF
KCKVNNKDLP SPIERTISKI KGLVRAPQVY ILPPPAEQLS RKDVSLTCLV
VGFNPGDISV EWTSNGHTEE NYKDTAPVLD SDGSYFIYSK LNMKTSKWEK
TDSFSCNVRH EGLKNYYLKK TISRSPGK[STOP]
**********************************************************************

[Sig-pep] MAVLGLLFCLVTFPSCVLS

[VH-region]
FR1:  QVQLKQSGPGLVQPSQSLSITCTVSGFSLT
CDR1: SYGVH
FR2:  WVRQSPGKGLEWLG
CDR2: VIWSGGDTDYNAAFIS
FR3:  RLSISKDNSKSQLFFKMNSLRATDTAIYYCAR
CDR3: NRGDIYYDFTYAMDY
FR4:  WGQGTSVTVSS

[CH-region]
CH:
AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK GYFPESVTVT WNSGSLSSSV
HTFPALLQSG LYTMSSSVTV PSSTWPSQTV TCSVAHPASS TTVDKKLEPS
GPISTINPCP PCKECHKCPA PNLEGGPSVF IFPPNIKDVL MISLTPKVTC
VVVDVSEDDP DVQISWFVNN VEVHTAQTQT HREDYNSTIR VVSTLPIQHQ
DWMSGKEFKC KVNNKDLPSP IERTISKIKG LVRAPQVYIL PPPAEQLSRK
DVSLTCLVVG FNPGDISVEW TSNGHTEENY KDTAPVLDSD GSYFIYSKLN
MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI SRSPGK[STOP]
```

FIG. 6B

m166 light chain

1. m166 light chain (k) complete mRNA sequence:

(From the transcriptional start point to the polyA tail)

```
ACACCCTTTG CTGGAGTCAG AATCACACTG ATCACACACA GTCATGAGTG
TGCTCACTCA GGTCCTGGCG TTGCTGCTGC TGTGGCTTAC AGGTGCCAGA
TGTGACATCC AGATGACTCA GTCTCCAGCC TCCCTATCTG CATCTGTGGG
AGAAACTGTC ACCATCACAT GTCGAGCAAG TGGGAATATT CAAAATTATT
TAGCATGGTA TCAGCAGACA CAGGGAAAAT CTCCTCAGCT CCTGGTCTAT
TCTGCAAAAA CCTTAGCAGA TGGTGTGCCA TCAAGGTTCA GTGGCAGTGG
ATCAGGAACA CAATATTCTC TCAAGATCAA CAGCCTGCAG CCTGAAGATT
TTGGGAGTTA TTACTGTCAA CATTTTTGGA GTACTCCGTA CACGTTCGGA
GGGGGGACCA AGCTGGAAAT AAAACGGGCT GATGCTGCAC CAACTGTATC
CATCTTCCCA CCATCCAGTG AGCAGTTAAC ATCTGGAGGT GCCTCAGTCG
TGTGCTTCTT GAACAACTTC TACCCCAAAG ACATCAATGT CAAGTGGAAG
ATTGATGGCA GTGAACGACA AAATGGCGTC CTGAACAGTT GGACTGATCA
GGACAGCAAA GACAGCACCT ACAGCATGAG CAGCACCCTC ACGTTGACCA
AGGACGAGTA TGAACGACAT AACAGCTATA CCTGTGAGGC CACTCACAAG
ACATCAACTT CACCCATTGT CAAGAGCTTC AACAGGAATG AGTGTTAGAG
ACAAAGGTCC TGAGACGCCA CCACCAGCTC CCCAGCTCCA TCCTATCTTC
CCTTCTAAGG TCTTGGAGGC TTCCCCACAA GCGACCTACC ACTGTTGCGG
TGCTCCAAAC CTCCTCCCCA CCTCCTTCTC CTCCTCCTCC CTTTCCTTGG
CTTTTATCAT GCTAATATTT GCAGAAAATA TTCAATAAAG TGAGTCTTTG
CAAAAAAAAA AAAAAAAAAA AAAAAAAAA
```

2. m166 light chain (k) amino acid complete sequence:

(From the start coden to the stop codon)

```
MSVLTQVLAL LLLWLTGARC DIQMTQSPAS LSASVGETVT ITCRASGNIQ
NYLAWYQQTQ GKSPQLLVYS AKTLADGVPS RFSGSGSGTQ YSLKINSLQP
EDFGSYYCQH FWSTPYTFGG GTKLEIKRAD AAPTVSIFPP SSEQLTSGGA
SVVCFLNNFY PKDINVKWKI DGSERQNGVL NSWTDQDSKD STYSMSSTLT
LTKDEYERHN SYTCEATHKT STSPIVKSFN RNEC[STOP]
```

[Sig-pep] MSVLTQVLALLLLWLTGARC

[VL-region]
FR1: DIQMTQSPASLSASVGETVTITC
CDR1: RASGNIQNYLA
FR2: WYQQTQGKSPQLLVY
CDR2: SAKTLAD
FR3: GVPSRFSGSGSGTQYSLKINSLQPEDFGSYYC
CDR3: QHFWSTPYT
FR4: FGGGTKLEIKR

[CL-region]
CL: ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL
NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC[STOP]

FIG. 7